

copy of alignment to Appl.

AAD07974

ID AAD07974 standard; cDNA; 1957 BP.

XX

DE Rice cysteinyl-tRNA synthetase cDNA clone rs11n.pk016.p18.

OS Oryza sativa.

XX

PN US6255090-B1. PARENT Appl.

XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PA (PION-) PIONEER HI-BRED INT INC.

XX

PI Famodu LO, Orozco EM, Rafalski JA;

XX

SQ Sequence 1957 BP; 599 A; 384 C; 470 G; 504 T; 0 other;

Alignment Scores:

Pred. No.:	1.3e-194	Length:	1957
Score:	2398.00	Matches:	452
Percent Similarity:	91.47%	Conservative:	41
Best Local Similarity:	83.86%	Mismatches:	38
Query Match:	76.42%	Indels:	8
DB:	22	Gaps:	3

US-09-846-589A-10 (1-599) x AAD07974 (1-1957)

CORN Qy ^{Seq 10} 57 SerProProSerAlaThrIleAlaGluAlaThrAlaPro---ProGlnLeuLeuLeuPhe 75
rice Db 45 TCCCCCTCCGCTCTCACGATGGCGGAGAGCGCGAAGCCGACGCCGAGCTGGAGCTCTTC 104
Qy 76 AsnSerPheThrLysArgGluGluProPheGlnProArgValGluGlyLysValGlyMet 95
Db 105 AACTCGATGACGAAGAAGAAGGAGCTCTTCGAGCCGCTTGTGGAGGGGAAGGTCCGCATG 164
Qy 96 TyrValCysGlyValThrProTyrAspPheSerHisIleGlyHisAlaArgAlaTyrVal 115
Db 165 TATGTGTGCGGCGTCACGCCCTACGACTTCAGCCACATCGGCCACGCCCGCGCCTACGTC 224
Qy 116 AlaPheAspValLeuTyrArgTyrLeuLysPheLeuGlyTyrGluValGluTyrValArg 135
Db 225 GCCTTCGACGTCCTCTACAGGTATCTTAAATTCTTGGGGTACGAGGTGAATATGTGCGC 284
Qy 136 AsnPheThrAspIleAspAspLysIleIleLysArgAlaAsnGluArgGlyGluThrVal 155
Db 285 AACTTCACTGATATTGATGACAAGATTATCAAACGAGCAAATGAAGCTGGTGAAACTGTA 344
Qy 156 ThrSerLeuSerSerGlnPheIleAsnGluPheLeuLeuAspMetThrGluLeuGlnCys 175
Db 345 ACTAGCTTGAGCAGCCGTTTATTAAATGAATTCCTTCTCGATATGGCTCAGCTCCAGTGC 404
Qy 176 LeuProProThrCysGluProArgValThrGluHisIleGluHisIleIleLysLeuIle 195
Db 405 TTACCCCAACTTGTGAGCCACGTGTGACGGATCACATTGAACATATTATAGAGTTGATA 464
Qy 196 ThrGlnIleMetGluAsnGlyLysAlaTyrAlaIleGluGlyAspValTyrPheSerVal 215
Db 465 ACCAAGATAATGGAGAATGGGAAAGCCTATGCTATGGAAGGAGATGTTTACTTTTCAGTT 524

Qy	216	GluSerPheProGluTyrLeuSerLeuSerGlyArgLysPheAspGlnAsnGlnAlaGly	235
		:::	
Db	525	GATACTTTCCCTGAGTATCTCAGTTTATCTGGAAGGAAGTTAGATCATAATCTTGCTGGT	584
Qy	236	AlaArgValAlaPheAspThrArgLysArgAsnProAlaAspPheAlaLeuTrpLysAla	255
		:::	
Db	585	TCGCGGGTTGCTGTGCGATACAAGAAAGCGGAACCTGCAGACTTTGCGCTGTGGAAGGCT	644
Qy	256	AlaLysGluGlyGluProPheTrpAspSerProTrpGlyArgGlyArgProGlyTrpHis	275
Db	645	GCTAAGGAAGGCGAACCTTTCTGGGATAGCCCATGGGGCCGTGGTAGACCAGGATGGCAT	704
Qy	276	IleGluCysSerAlaMetSerAlaHisTyrLeuGlyHisValPheAspIleHisGlyGly	295
Db	705	ATTGAATGCAGTGAATGAGTGCTCATTATTTAGGACATGTGTTTGATATCCATGGTGA	764
Qy	296	GlyLysAspLeuIlePheProHisHisGluAsnGluLeuAlaGlnSerArgAlaAlaTyr	315
Db	765	GGGAAAGATCTGATATTTCTCATCATGAGAATGAGCTTGCTCAGAGCCGGGCAGCTTAT	824
Qy	316	ProAspSerGluValLysCysTrpMetHisAsnGlyPheValAsnLysAspAspLysLys	335
		:::	
Db	825	CCAGAAAGTGAGGTCAAATGTTGGATGCACAATGGGTTTGTTAACAAGGATGATCAGAAA	884
Qy	336	MetAlaLysSerAspAsnAsnPhePheThrIleArgAspIleIleAlaLeuTyrHisPro	355
		:::	
Db	885	ATGTCAAAGTCAGATAAAAATTTCTTCACAATCCGAGATATTATTGATCTGTACCATCCC	944
Qy	356	MetAlaLeuArgPhePheLeuMetArgThrHisTyrArgSerAspValAsnHisSerAsp	375
Db	945	ATGGCTTTGAGGTTTTTCTCTGATGCGCACACATTACAGAGGAGATGTGAATCACTCTGAC	1004
Qy	376	GlnAlaLeuGluIleAlaSerAspArgValTyrTyrIleTyrGlnThrLeuTyrAspCys	395
		:::	
Db	1005	AAAGCACTTGAGATAGCATCTGATCGTGTCTACTACATATATCAGACTTTATATGACTGT	1064
Qy	396	GluGluValLeuAlaThrTyrArgGluGluGlyThrSerLeuProValProSerGluGlu	415
Db	1065	GAGGAAGTGTGTCTCAATATCGTGGAGAGAAATATCTCTGTCCCGGTCCCTGTTGAGGAA	1124
Qy	416	GlnAsnLeuIleGlyLysHisHisSerGluPheLeuLysHisMetSerAsnAspLeuLys	435
		:::	
Db	1125	CAAGATATGGTTAACAAGCACCATTTCAGAAATCTTGAATCTATGGCGGATGATCTTAGA	1184
Qy	436	ThrThrAspValLeuAspArgCysPheMetGluLeuLeuLysAlaIleAsnSerSerLeu	455
Db	1185	ACAACAGATGTTCTGGATGGC---TTTACTGACTTGCTGAAGGCAATTAACAGCAATTTG	1241
Qy	456	AsnAspLeuLysLysLeuGlnGlnLysIleGluGlnGlnLysLysLysGlnGlnGlnGln	475
Db	1242	AATGATTTTAAGAAGTTGCAACAGAAGCTAGAGCAGCAAAG-----	1283
Qy	476	LysLysGlnGlnGlnGlnLysGlnGlnGlnGlnLysGlnGlnGlnLeuGlnLysGlnPro	495
Db	1284	AAGAAACAACAACAGCAGAAGCAGCAGAAGCAAAAGCAGCAGCAGGCACAGAAACAACCA	1343

Qy 496 GluAspTyrIleGlnAlaLeuIleAlaLeuGluThrGluLeuLysAsnLysLeuSerIle 515
 |||:::|||||||||||||::: |||||||||||||||:::|||||||||:::|||||
 Db 1344 GAAGAATATATTCAAGCTATGTTTGCACCTTGAGACAGAAATTAAAAATAAAATATCTATC 1403

Qy 516 LeuGlyLeuMetProSerSerSerLeuAlaGluValLeuLysGlnLeuLysAspLysSer 535
 ||||||||||||||| ||||||||||||||| |||||||||||||||:::
 Db 1404 CTTGGTCTGATGCCACCTTCTTCCTTGGCAGAGGCACTGAAGCAACTTAAGGATAAAGCT 1463

Qy 536 LeuLysArgAlaGlyLeuThrGluGluGlnLeuGlnGluGlnIleGluGlnArgAsnVal 555
 |||||||||||||||||||| ||||||||||||||||
 Db 1464 TTGAAGAGAGCAGGGTTGACTGAAGAAGTGTTCAGGAGCAAATTGAGCAGAGAACTGCT 1523

Qy 556 AlaArgLysAsnLysGlnPheGluIleSerAspGlyIleArgLysAsnLeuAlaThrLys 575
 |||||||||||||||||||:::||||| ||||||| ||| ::|||
 Db 1524 GCAAGGAAAAACAAGCAGTTTGATGTGTCTGACCAAATCAGGAAACAGCTAGGCAGCAAA 1583

Qy 576 GlyIleAlaLeuMetAspGluProSerGlyThrValTrpArgProCysGluProGlu 594
 |||||||||||||||||||:::||||||||||||||||||
 Db 1584 GGCATAGCCCTCATGGATGAACCTACTGGTACAGTATGGAGACCATGCGAGCCAGAG 1640

copy of alignment to Applicant

AAD07975
 ID AAD07975 standard; cDNA; 2183 BP.
 XX
 DE Soybean cysteinyl-tRNA synthetase cDNA clone sf11.pk0013.f9.
 XX
 OS Glycine max.
 XX
 PN US6255090-B1.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Famodu LO, Orozco EM, Rafalski JA;
 XX
 SQ Sequence 2183 BP; 621 A; 411 C; 485 G; 666 T; 0 other;

Alignment Scores:

Pred. No.:	1.79e-115	Length:	2183
Score:	1470.00	Matches:	301
Percent Similarity:	65.65%	Conservative:	85
Best Local Similarity:	51.19%	Mismatches:	146
Query Match:	46.85%	Indels:	57
DB:	22	Gaps:	8

US-09-846-589A-10 (1-599) x AAD07975 (1-2183)

Seq 9
CORN

soybean

Qy	7	SerThrThrProLeuSerProProProProProProGlnIleProPheArgValCysLeu	26
Db	115	TCCCTCACTCCGCTCCACCCAGACTCCACGCCGCCA-----	150
Qy	27	AlaSerGlyAlaSerArgLeuAlaArgAlaThrThrMetAlaGluGluValGlnAlaPro	46
Db	151	TCTTCAGGAGCAAAACTTTTCTTTTTCGCC-ACCTCGTCC-----CCGCCG	197
Qy	47	LeuSerAlaThrMetAlaLysGluAlaGlnSerProProSerAlaThrIleAlaGluAla	66
Db	198	TTGACG-----GCGGAGAAGGGTTGCGGCAAAATCCGACGCCGAGTGT	239
Qy	67	ThrAlaProProGlnLeuLeuLeuPheAsnSerPheThrLysArgGluGluProPheGln	86
Db	240	CCCACCTTGCCGAGGTGTGGCTGCACAACACCATGAGTAGGACGAAGGAAGTCTTCAA	299
Qy	87	ProArgValGluGlyLysValGlyMetTyrValCysGlyValThrProTyrAspPheSer	106
Db	300	CCCAAAGTGGAATCCAAAGTGGGAATGTACGTGTGCGGCGTCACCGCTTATGATCTTAGC	359
Qy	107	HisIleGlyHisAlaArgAlaTyrValAlaPheAspValLeuTyrArgTyrLeuLysPhe	126
Db	360	CATATTGGACACGCTCGCGTATACGTCAATTTGACCTTCTTTACAGATACTTTAAGCAT	419
Qy	127	LeuGlyTyrGluValGluTyrValArgAsnPheThrAspIleAspAspLysIleIleLys	146
Db	420	TTGGGATTGAAGTCTGTTATGTTTCGCAATTTCACTGACGTAGATGACAAGATAATTGCT	479
Qy	147	ArgAlaAsnGluArgGlyGluThrValThrSerLeuSerSerGlnPheIleAsnGluPhe	166
Db	480	AGAGCAAAGGAGTTAGGAGAAGATCCAATCAGTTTGTGAGCTGGCGCTATTGTGAAGAGTTC	539

Qy 167 LeuLeuAspMetThrGluLeuGlnCysLeuProProThrCysGluProArgValThrGlu 186
 Db 540 TGTCAAGACATGGTAACCTCTTAATTGTCTGTCTCCCTCTGTGGAACCAAAGGTCTCAGAG 599
 Qy 187 HisIleGluHisIleIleLysLeuIleThrGlnIleMetGluAsnGlyLysAlaTyrAla 206
 Db 600 CACATGCCCCAAATCATTGATATGATTGAGAAGATCCTTAATAATGGGTATGCCTACATT 659
 Qy 207 IleGluGlyAspValTyrPheSerValGluSerPheProGluTyrLeuSerLeuSerGly 226
 Db 660 GTTGATGGGGATGTGTACTTTAATGTAGAAAAATTTCCAGAATATGGGAACTATCTAGT 719
 Qy 227 ArgLysPheAspGlnAsnGlnAlaGlyAlaArgValAlaPheAspThrArgLysArgAsn 246
 Db 720 CGAGATCTAGAAGATAATCGAGCTGGTGAGAGGGTTGCAGTTGATTCTAGAAAGAAAAAT 779
 Qy 247 ProAlaAspPheAlaLeuTrpLysAlaAlaLysGluGlyGluProPheTrpAspSerPro 266
 Db 780 CCTGCTGATTTTGCTCTTTGGAAGTCTGCAAGCCAGGGGAGCCATTTTGGGAGAGTCCC 839
 Qy 267 TrpGlyArgGlyArgProGlyTrpHisIleGluCysSerAlaMetSerAlaHisTyrLeu 286
 Db 840 TGGGGTCTCTGGAAGACCTGGGTGGCATATTGAATGCAGTGCCATGAGTGCAGCTTATCTT 899
 Qy 287 GlyHisValPheAspIleHisGlyGlyGlyLysAspLeuIlePheProHisHisGluAsn 306
 Db 900 GGTTACTCTTTTGATATCCATGGTGGAGGAATCGACCTTGTTTCTCACCATGAGAAT 959
 Qy 307 GluLeuAlaGlnSerArgAlaAlaTyrProAspSerGluValLysCysTrpMetHisAsn 326
 Db 960 GAAATTGCTCAGAGTTGTGCTGCATGTAAGAAAAGTGATATAAGTATATGGATGCACAAT 1019
 Qy 327 GlyPheValAsnLysAspAspLysLysMetAlaLysSerAspAsnAsnPhePheThrIle 346
 Db 1020 GGTTTTGTCAACATTGACTCTGTGAAAATGTCAAATCTTTGGGGAATTTTTCACAATA 1079
 Qy 347 ArgAspIleIleAlaLeuTyrHisProMetAlaLeuArgPhePheLeuMetArgThrHis 366
 Db 1080 CGTCAGTTATAGACGTTTACCATCCACTGGCCTTGAGATATTTTTTGATGAGCGCACAT 1139
 Qy 367 TyrArgSerAspValAsnHisSerAspGlnAlaLeuGluIleAlaSerAspArgValTyr 386
 Db 1140 TATCGATCTCCTATTAATACTCAAAATATACAGCTCGAAAGTGCTTCAGACCGTGTTTTT 1199
 Qy 387 TyrIleTyrGlnThrLeuTyrAspCysGluGluValLeuAlaThrTyrArgGluGluGly 406
 Db 1200 TATATATATGAGACATTACATGAATGTGAAAGCTTTTTGAATCAGCATGATCAGAGGAAG 1259
 Qy 407 ThrSerLeuProValProSerGluGluGlnAsnLeuIleGlyLysHisHisSerGluPhe 426
 Db 1260 GATTCC-----ACCCACCGGATACTTTGGATATTATTGATAAGTTCCACGATGTTTTT 1313
 Qy 427 LeuLysHisMetSerAsnAspLeuLysThrThrAspValLeuAspArgCysPheMetGlu 446
 Db 1314 TTGACCTCAATGTGCGATGATCTTCACTCCAGTTGTATTG----- 1355

Qy 447 LeuLeuLysAlaIleAsnSerSerLeuAsnAsp---LeuLysLysLeuGlnGlnLysIle 465
 Db 1356 -----GCTGGAATGTCTGATCCATTAAAATCAATCAATGATTGCTG 1397
 Qy 466 GluGlnGlnLysLysLysGlnGlnGlnGlnLysLysGlnGlnGlnGlnLysGlnGlnGln 485
 Db 1398 CATGCTCGTAAGGGGAAAAACAACAATTTCTGA----- 1430
 Qy 486 GlnLysGlnGlnGlnLeuGlnLysGlnProGluAspTyrIleGlnAlaLeuIleAlaLeu 505
 Db 1431 -----ATCGAATCACTATCAGCTTTG 1451
 Qy 506 GluThrGluLeuLysAsnLysLeuSerIleLeuGlyLeuMetProSerSerSerLeuAla 525
 Db 1452 GAGAAGAGCGTCAGGGATGTCCTTACTGTTTTAGGACTTATGCCT---GCAAGTTACTCT 1508
 Qy 526 GluValLeuLysGlnLeuLysAspLysSerLeuLysArgAlaGlyLeuThrGluGluGln 545
 Db 1509 GAGGTTTTGCAGCAGCTTAAGGTAAAAGCTTTAAACGTGCAAACCTTACGGAAGAAGAA 1568
 Qy 546 LeuGlnGluGlnIleGluGlnArgAsnValAlaArgLysAsnLysGlnPheGluIleSer 565
 Db 1569 GTCTTGCAAAAATTGAAGAACGGGCTACTGCTAGAATGCAAAGGAGTATGCTAAATCG 1628
 Qy 566 AspGlyIleArgLysAsnLeuAlaThrLysGlyIleAlaLeuMetAspGluProSerGly 585
 Db 1629 GATGCAATCAGGAAGGATTTGGCTGTACTTGGTATTACTCTTATGGACAGTCCAAATGGC 1688
 Qy 586 ThrValTrpArgProCysGluPro 593
 Db 1689 ACAACTTGGAGGCCTGCCATTTCCT 1712

1